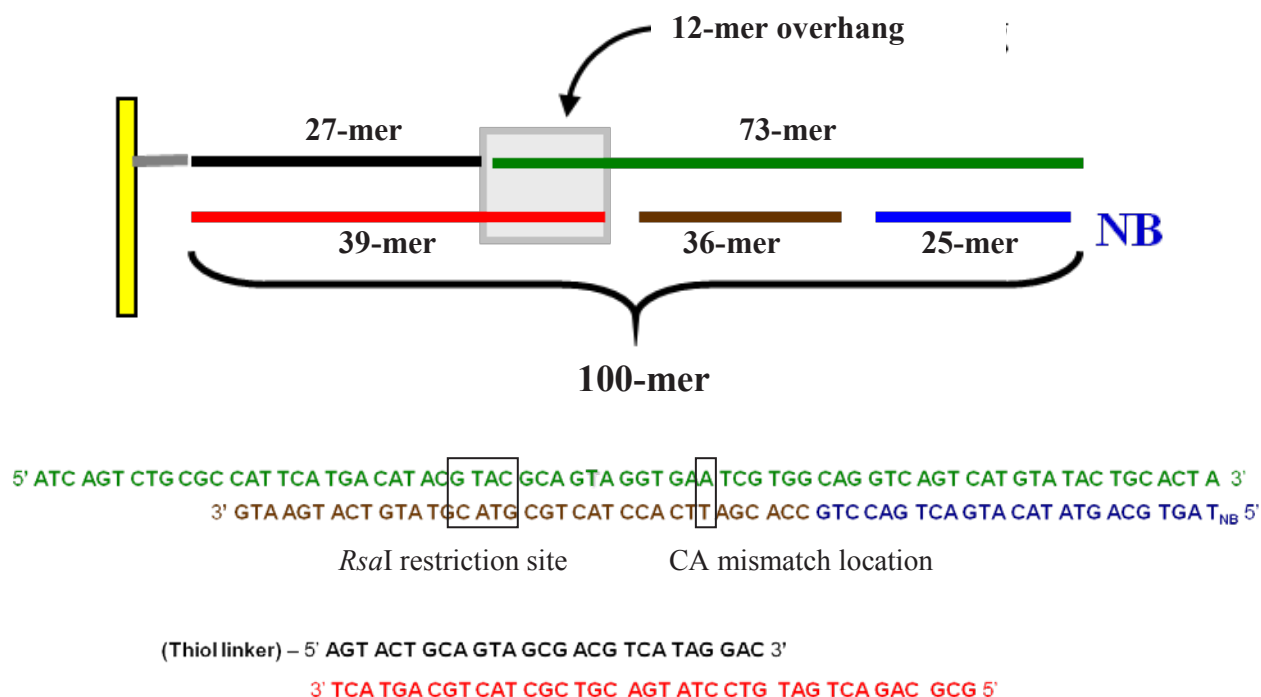


**Supporting Information:**  
**DNA Charge Transport over 34 nm**

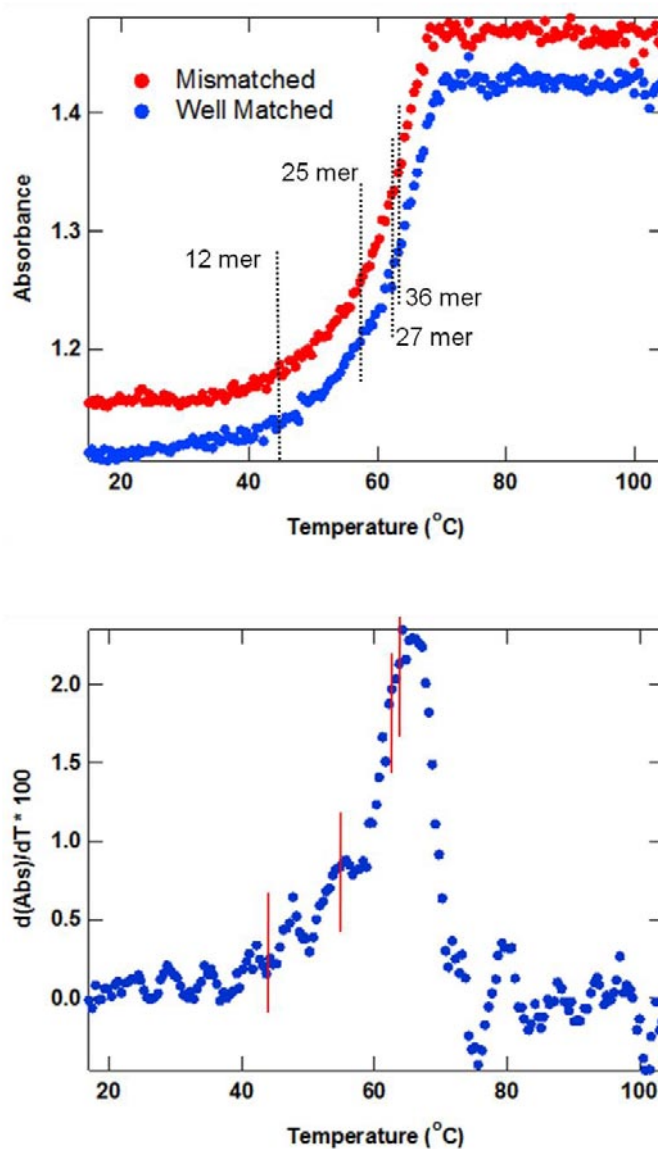
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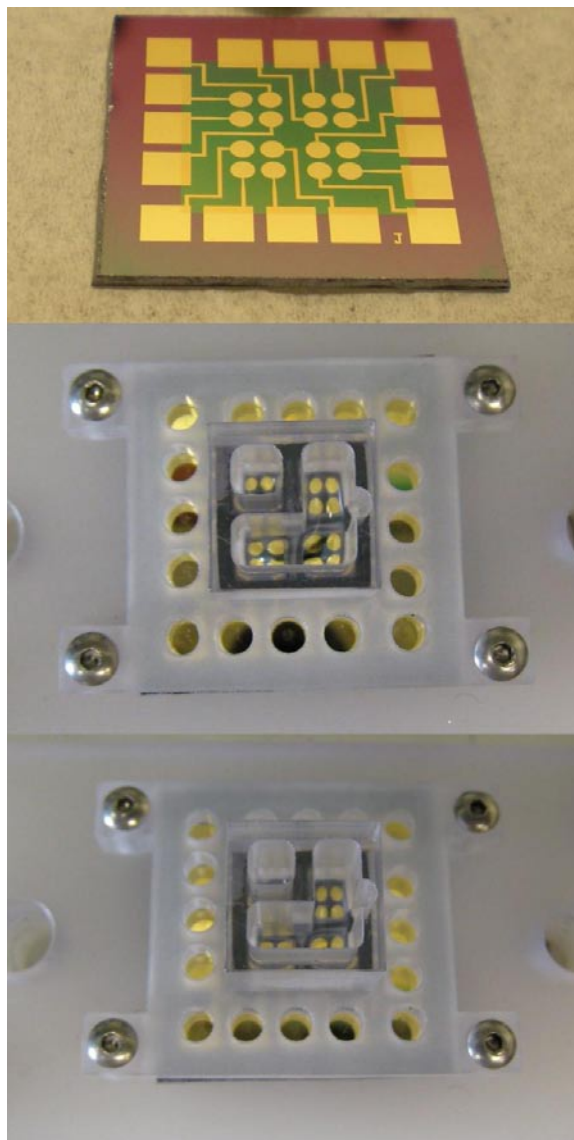
Email: [jkbarton@caltech.edu](mailto:jkbarton@caltech.edu)



**Supporting Figure 1.** Assembly of the well matched 100-mer double stranded DNA sequence. The overall duplex is composed of five single stranded DNA segments. The two double stranded DNA segments shown above are joined by complementary 12 base overhands, or “sticky ends”. This leads to four melting transitions. The positions of the *Rsa*I restriction site and CA mismatch, both within the central 36-mer, are indicated.



**Supporting Figure 2.** Melting temperature analysis of well matched (blue) and mismatched (red) 100-mers. (Upper) Absorbance at 260 nm versus temperature for well matched and mismatched 100-mers. The vertical lines note the 4 anticipated melting transitions from calculations (IDT Oligo Analyzer). (Lower) The first derivative of absorbance versus temperature for the well matched 100-mer. The red vertical lines note the calculated melting transitions.



**Supporting Figure 3.** (Top) Picture of the 16 electrode chips used for electrochemical analysis. (Middle and Bottom) Picture of the chip and well assembly with one isolated deep well, used for the *RsaI* restriction endonuclease experiment. The chip clamp has three shallow wells enclosed by a deep well and one isolated deep well. The three shallow wells (volume  $\sim 25 \mu\text{L}$ ) permit assembly of various DNA monolayers from solution on the quadrants of the chip, while the interconnected deep well permits all three to be exposed to the same analyte-bearing solution. For the *RsaI* experiment, the enzyme was added to these three interconnected quadrants, while the quadrant isolated with the deep well was maintained free of *RsaI*. The reference and counter electrodes (not shown) must be transferred back and forth between the wells, or separate reference and counter electrodes must be used.